

117: qb_08148: *
118: qb_08149: *
119: qb_08150: *
120: qb_08151: *
121: qb_08152: *
122: qb_08153: *
123: qb_08154: *
124: qb_08155: *
125: qb_08156: *
126: qb_08157: *
127: qb_08158: *
128: qb_08159: *
129: qb_08160: *
130: qb_08161: *
131: qb_08162: *
132: qb_08163: *
133: qb_08164: *
134: qb_08165: *
135: qb_08166: *
136: qb_08167: *
137: qb_08168: *
138: qb_08169: *
139: qb_08170: *
140: qb_08171: *
141: qb_08172: *
142: qb_08173: *
143: qb_08174: *
144: qb_08175: *
145: qb_08176: *
146: qb_08177: *
147: qb_08178: *
148: qb_08179: *
149: qb_08180: *
150: qb_08181: *
151: qb_08182: *
152: qb_08183: *
153: qb_08184: *
154: qb_08185: *
155: qb_08186: *
156: qb_08187: *
157: qb_08188: *
158: qb_08189: *
159: qb_08190: *
160: qb_08191: *
161: qb_08192: *
162: qb_08193: *
163: qb_08194: *
164: qb_08195: *
165: qb_08196: *
166: qb_08197: *
167: qb_08198: *
168: qb_08199: *
169: qb_08200: *
170: qb_08201: *
171: qb_08202: *
172: qb_08203: *
173: qb_08204: *
174: qb_08205: *
175: qb_08206: *
176: qb_08207: *
177: qb_08208: *
178: qb_08209: *
179: qb_08210: *
180: qb_08211: *
181: qb_08212: *
182: qb_08213: *
183: qb_08214: *
184: qb_08215: *
185: qb_08216: *
186: qb_08217: *
187: qb_08218: *
188: qb_08219: *
189: qb_08220: *

190: qb_08221: *
191: qb_08222: *
192: qb_08223: *
193: qb_08224: *
194: qb_08225: *
195: qb_08226: *
196: qb_08227: *
197: qb_08228: *
198: qb_08229: *
199: qb_08230: *
200: qb_08231: *
201: qb_08232: *
202: qb_08233: *
203: qb_08234: *
204: qb_08235: *
205: qb_08236: *
206: qb_08237: *
207: qb_08238: *
208: qb_08239: *
209: qb_08240: *
210: qb_08241: *
211: qb_08242: *
212: qb_08243: *
213: qb_08244: *
214: qb_08245: *
215: qb_08246: *
216: qb_08247: *
217: qb_08248: *
218: qb_08249: *
219: qb_08250: *
220: qb_08251: *
221: qb_08252: *
222: qb_08253: *
223: qb_08254: *
224: qb_08255: *
225: qb_08256: *
226: qb_08257: *
227: qb_08258: *
228: qb_08259: *
229: qb_08260: *
230: qb_08261: *
231: qb_08262: *
232: qb_08263: *
233: qb_08264: *
234: qb_08265: *
235: qb_08266: *
236: qb_08267: *
237: qb_08268: *
238: qb_08269: *
239: qb_08270: *
240: qb_08271: *
241: qb_08272: *
242: qb_08273: *
243: qb_08274: *
244: qb_08275: *
245: qb_08276: *
246: qb_08277: *
247: qb_08278: *
248: qb_08279: *
249: qb_08280: *
250: qb_08281: *
251: qb_08282: *
252: qb_08283: *
253: qb_08284: *
254: qb_08285: *
255: qb_08286: *
256: qb_08287: *
257: qb_08288: *
258: qb_08289: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

[illegible]

Db	369	ACAAATCAAGCTGCTTAAATTAATTATTATGGCAGAGAGAAAATTAACCATCGACTGAAGG	428
QY	594	tttctgcacatcagaaattatcatltaqatcattacttggaagaattcttatccgtctctctata	654
Dbb	429	TTTTCGGGTGCGAAGATACAATCACATACTTGAGAGATCTTTAACTGTCCTTAATA	488
QY	654	aagcattcagatltggaccacgaatgattcttcagatcgatgagacacgccctccgc	709
Ddb	489	AGCACTTATGCTGATGAGCCACCTACCTATCTTTTATATATAGTAGATGATGCTGCTC	544
RESULT	5		
LACUS	AM465562	493 bp	mRNA EST 24 FEB 2000
DEFINITION	Bp230019810A2 Soares normalized bovine placenta Bos taurus cDNA clone Bp230019810A2 5' mRNA sequence.		
ACCESSION	AM465562		
VERSION	AM465562.1	GI:7035667	
KEYWORDS	EST.		
SOURCE	COW.		
ORGANISM	Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetozoa; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; bovinae; Bos. 1 (bases 1 to 493) Lewin,H.A., Soares,M.B., Rehboz,M., Pardinas,J., Liu,L. and Larson, J.L.H.		
REFERENCE	BOVINE ESTS Unpublished (2000)		
AUTHORS	Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Dynamics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel.: 217 333 5998 Fax: 217 244 5617 Email: h-lewin@uiuc.edu		
TITLE	Funding for cattle EST sequencing was provided by The USDA National Research Initiative, Animal Genome Resource Grant AR-94-1205-B5-44 to H. A. Lewin and J. E. Womack. Basic Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmed g: Cross-match from Washington University Genome Center PHRAP suite. Sequences submitted are vector free and at least 200 bp in length. PCR Primers FORWARD: TAATACGCATTCATATACG REVERSE: ATTATCCCTCACTTAAG Insert Length: 493 Std Error: 0.00 Plate: Bp230019810 Row: A Column: 2 Seq Primer: AGCGCATCAATTCATTCACGA High quality sequence stop: 493. Location/Qualifiers 1..493 /organism:"bos taurus" /db_xref:"taxon:9913" /clone="Bp230019810A2" /clone_lib:"Soares normalized bovine placenta" /sex:"female" /lab_host:"DHIBR" /note:"Organ: placenta; Vector: pUT7pac; Site: 1; ECORI: Site: 2; NotI: The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Ronaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9) : 791-806. "		
BASE COUNT	120 a	111 c	149 g
ORIGIN	124 t		
QUALITY MATCH	53.7%	Score 438.6;	DB 116; Length 493;
Best Local Similarity	94.1%	Pred No. 7	Ac-112;
Matches 459;	Conservative	0;	Mismatches 34;
Indels	0;	Gaps	0;
477	gcccgaagatcttgatcatgacgatctgaagacacccatgattcttggaagacattaca	546	

Db 1 GACCCGAGGTGTGTCACCATGACGAAAGCTCCAGTGTGTGGAGAGCACTTACA 60
 QY 537 acagagccctttagacatctactagcccaagcaagaataatctacgtctcgccttagcgttt 596
 Db 61 ACAGAGCCCTCTTAGACATATTATTATGCAAGAGCAAAATTACCGTCGCTGACGGCTTT 120
 QY 597 tccgcgtcgaagaatacatcttgaacatctacttgaagagatctctaaagctctgctaataagc 656
 Db 121 TCGCCGTCGGAGAGTACATTGAGCATTAAGTCTGACGAGCTTCTTAAGCTCTGCTAATAAGC 180
 QY 657 acttaatgatttgcacacagatcatcttcttaacatgagtgagagagctctcgaagatgc 716
 Db 181 ACTCATAGTGTGCGCCAGCCGCTCATCTTTATATCATGATGATGATGATGATGATGATGATG 240
 QY 717 ctgttagagagcttggagccctctgcgcctcttcaagatgcttggagtgatgaacccgagagga 776
 Db 241 CTGTGATAGATGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 QY 777 ggtgagagagcttgaacatcttgaacatcttgaacatcttgaacatcttgaacatcttgaacatct 836
 Db 301 GGTGAGAGAGCATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 QY 837 tccagcttgaagcttgaacatcttcttcttgaacatcttgaacatcttgaacatcttgaacatct 896
 Db 361 TCCAGCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 897 tccagcttgaagcttgaacatcttcttcttgaacatcttgaacatcttgaacatcttgaacatct 956
 Db 421 TTGGGCTGGAGAGCCCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAGCTGCGGAG 480
 QY 957 atcccttagat 969
 Db 481 ATCCCATGACCTT 493

RESULT 6
 AM463741 479 bp mRNA EST 24-FEB-2000
 LOCUS BP230013H10C8 Soares normalized bovine placenta Bos taurus cDNA
 DEFINITION
 ACCESSION AM463741
 VERSION AM463741.1 GI:7033909
 KEYWORDS EST.
 SOURCE cDNA.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 479)
 AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,
 J.O.H.
 TITLE Bovine ESTs
 JOURNAL Unpublished (2000)
 COMMENT Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Maddigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross-match from Washington University Genome Center PHRAP suite.
 Sequences submitted are vector free and at least 200 bp in length.
 PCR Primers
 FORWARD: TAATAGCATGCTATATGCG
 BACKWARD: ATTACCTTACTAAAG
 Insert Length: 479 Std Error: 0.00
 Plate: BP230013B10 row: G column: 8
 Seq primer: AGCGATAACATTTACACAGCA

FEATURES High quality sequence stop: 479.
 source location/Qualifiers
 1..479
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BP230013B10G8"
 /sex="female"
 /lab_host="DH10H"
 /note="Organ: Placenta; Vector: pT731ag; Site_: Prok1;
 Site_2: Not1: The cDNA library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996). Genome Research 6(9): 791-806."

HASH COUNT 142 a 102 c 122 g 113 t
 ORIGIN

Query Match 32.6%; Score 424.4; DB 116; Length 479;
 Best local similarity 94.0%; Pred. No. 6,9e-108;
 Matches 453; Conservative 0; Mismatches 26; Indels 4; Gaps 1;

QY 270 acagccagagagctcttcttctgataaacatcaaaagccagagatgaatgagc 329
 Db 1 ACAGCCAGAGAGCTCTTCTTCTGATTAACCCATCAAAAGCCAGAGT---TGTG 57
 QY 330 gcaagcaatcagaagagcttgaatgcttccagatgaatttaacaaatgtaacaaag 389
 Db 58 GCAGCAGCATTCGAAGAGGCTGCTGCTTCCGAGATGCTTTAACAAATGATACATGAA 117
 QY 390 aaatgaagagcttaagcgaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaag 449
 Db 118 AAGATGAGCATTAAGCAGAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 177
 QY 450 tategagctgttcaaacccatttaaacgacctgaagcttgaatgaatgaatgaatgaatgaatga 509
 Db 178 TATGAGAGCTGCTTCAACCCATTTAAAGCCCGCAGAGTTTGATGATGATGATGATGATGATG 247
 QY 510 caccctgagtgaggaagaggaacttaacaaagagagagctcttaacaaatgtaacaaag 569
 Db 238 CTCAGAGCTGCTGGAAGGCTGCTGCTTCCGAGATGCTTTAACAAATGATACATGAA 297
 QY 570 aaaaaatlaacgctcgcgtctgaacatcttgcgcgtcgaagaaatgaatgaatgaatgaatga 629
 Db 298 AGAAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 357
 QY 630 agagatcttaacgctcgcgtctgaacatcttgcgcgtcgaagaaatgaatgaatgaatgaatga 689
 Db 358 AGAGTCTTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 417
 QY 690 tcatgtgaagagctctcagagatgcttgaatgaatgaatgaatgaatgaatgaatgaatga 749
 Db 418 TCATGTAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 477
 QY 750 aa 751
 Db 478 AA 479

RESULT 7
 AM464433 475 bp mRNA EST 24-FEB-2000
 LOCUS BP230013H20C5 Soares normalized bovine placenta Bos taurus cDNA
 DEFINITION
 ACCESSION AM464433
 VERSION AM464433.1 GI:7034601
 KEYWORDS EST.
 SOURCE cDNA.
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 475)

[illegible]

	DB	256	AAGTAATGATTGTCAAGAATAAAACCTAATTCGGTCAACTGCAGTTGGTCCAACCGTGCTCATGG	315
OY	249	TGTTGTTTTGAAGatatactccacagccccaaaggcctttgttcgagttaadggcaactcaa		308
Db	316	TTGTGTTTGGGAAATATATATCACAAGCCATCACAGGCCCTTTGTCTTGAAATCAAACCATCAAA		475
OY	309	GAAAATCCAagaattcgatgcgcgaaccagcatcttgaaaagagctgatgatttcccgaatatggt		468
Db	376	GAAAACTACAAAGT---TGTTGGTAGCACCATTTACAAAGGCGTGGTGCGCTTCCAGAGATGCT		432
OY	369	TAcCaAtAgTtAccGaGaGaGaGaTaTgaGaGeMtagaGqaqaaGaGaGaGaGaGaGaGaqq		428
Db	433	TTACCAATGCTTACTATATATTAAGACAGATCAACACATTAAGAGAAAGAAAGAAAGAAAGG		492
OY	429	aadaacaagatcaccttaaagctatccgaatgattcaaccttatccaactttaaacgccctgaqg		485
Db	493	AAAGCAAAAGCAAGCTTAAGCTATGCACTATGGTTCATCAATTTAAACATCTCCAGAG; 549		
RESULT 11				
Locus	HGI74143	1094 bp	mRNA	FEST
DEFINITION	6023343142E1 NC_109AP_Mamm Mus musculus cDNA clone IMAGE:447334			57
ACCESSION	BH174143			
VERSION	BH174143.1 GI:1260846			
KEYWORDS	EFT.			
SOURCE	house mouse;			
ORGANISM	Mus musculus			
REFERENCE	Eukaryotid Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathit Muridae; Murinae; Mus. 1 (bases 1 to 1094)			
AUTHORS	NIH-MRC http://www.ncbi.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGCL) Unpublished (1999)			
JOURNAL	Contact: Robert Strausberg, Ph.D., Email: rstraub@mail.nih.gov Tissue procurement: Gilbert Smith, Ph.D., cDNA library preparation: Life Technologies, Inc., cdna library Arrayed by: The I.M.A.G.E Consortium (LMML) dna sequencing by: Incyte Genomics, Inc, clone distribution: MGC clone distribution information can be found through the I.M.A.G.E Consortium/LMML at: http://image.llnl.gov plate: LMML0253 row: P column: Q7 High quality sequence stop: 662.			
COMMENT				
FEATURES				
SOURCE	Location/Organisms 1..1094 /organism "Mus musculus" /strain "FVB/N"			
	/db_xref "taxon:10090"			
	/clone "IMAGE:4457334"			
	/clone_lib "NCI_CGP_Mam1"			
	/tissue_type "tumor, biopsy sample"			
	/dev_stage "3 months, virgin"			
	/lab_host "PH10H"			
	/note "Organ: mammary; Vector: pCMV-SportVec Site_1: SalII Site_2: NotI; cloned unidirectionally. Primer: oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"			
BASE COUNT	325 A 288 C 291 G 190 T			
ORIGIN				
Query Match	27.5%	Score 358.67	DB 174:	Length 1094;
Best Local Similarity	74.5%	Pred. No. 2, 5e-89;		
Matches	451 Conservative	Q7 Mismatches 154;	Indels	Q7 Gaps 0
OY	371	dacaaatgattaccaaatdaaagataaagagctgtagacacgaagaagaaacaaaaaagaa		430
Db	100	ACCCACAGGTTATTCACAGAACCAACGTTACAGAGACGACGACAGACAAAGGCTGACAAATGGACAGT		159

```

QY 431 gacaaagaaagccttaagatcagactcgtcctcaacccattaaagccctgaagttctg 490
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 160 cccatttgaaagacccctagctatgagcactgttcaatccaaagacccggcgatgtttg 219
QY 491 actaagagatgaagacccctgagctgaggaagcagcttacagagacgctctta 550
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 220 acagtgaccccgtagagaccccgcatgtgttgaaagacattatgacacacactctgctg 279
QY 551 gacgattactaacgcaagaaatfacgctgagcctgaagcttctgctcgcgaaga 610
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 280 gaaatgactatgacccacacagaaactcactgtggagctgcacagtgtgtgtggaag 339
QY 611 tacattgacatctacttgagagatctctaacgctctgtaalaagcacttcagttgac 670
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 340 tgcattgacattacttacaagacatttgcagctgctgacatgacttcatgtgtgac 399
QY 671 gacgaatcattcttactgaagcagcagctctcagagatgcttctgtagagctg 730
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 400 catggcgatcatattttactcatgatacagacacactcccgatgctctgacactg 459
QY 731 gacccctcagcctccttcaaaagtttgaagcagcctgagagagatgagagagctc 790
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 460 aacccctcactacattcttacaagcttgcagatcagctcagaaagagctgcagatattc 519
QY 791 agcagtgctcagatgaagccatcgaggagacacatcgtgcccacatccagcgtagatt 850
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 520 accatgactcgcatagaacacacattgagagacacatcctgacacacacacacacacg 579
QY 851 gactcctcctcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 910
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 580 gacttcctcctcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 639
QY 911 ctggatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 970
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 640 ctggatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 699
QY 971 accta 975
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 700 accta 704

```

```

RESULT 12
AV666881/c
LOCUS AV666881 399 bp mRNA EST 25-AUG-2000
DEFINITION AV666881 Bos taurus adipocyte cell line Bos taurus cDNA clone
E1AD021G06 3', mRNA sequence.
ACCESSION AV666881
VERSION AV666881.1 GI:9925911
KEYWORDS EST.
SOURCE EST.
ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
            1 (bases 1 to 399)
AUTHORS Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and
            Suzuki, H.
TITLE bovine cDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
            Animal Genetics Division
            Shitakawa Institute of Animal Genetics
            Odakura, Nishigo, Nishi-Shitakawa, Fukushima 961-8061, Japan
            Tel: 81-248-25-5641
            Fax: 81-248-25-5725
            Email: kazusugi@acocoa.ocn.ne.jp
FEATURES
            Single pass sequencing.
            This clone was obtained from a polyA-deleted cDNA library.
            location=Qualifiers
            1..399
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone="E1AD021G06"

```

```

/cclone.lib="Bos taurus adipocyte cell line"
/cell_type="an adipocyte cell line"
/lab_host="DH108"
/Note="Vector: pCL1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"
BASE COUNT 102 a 113 c 89 g 95 t
ORIGIN

```

```

Query Match 25.5%: Score 331.8; DB 32; Length 399;
Best Local Similarity 92.7%; Pval. No. 5.8e-82;
Matches 370; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

```

```

QY 592 gatttcgcccgc- ggaagataacattgaacatctacttgaagaaattcttaacgtctgta 650
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 399 gatttcgcccgc- ggaagataacattgaacatctacttgaagaaattcttaacgtctgta 340
QY 651 ataagac- ttcatgatttgacacacacacacacacacacacacacacacacacacacac 709
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 339 ataagac- ttcatgatttgacacacacacacacacacacacacacacacacacacacac 280
QY 710 agaatgctcttgaatgaagctgaagcctcctcagcctcctcaaaatglttgaagcagcct 769
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 279 agaatgctcttgaatgaagctgaagcctcctcagcctcctcaaaatglttgaagcagcct 220
QY 770 gagaagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 829
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 219 gagaagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 160
QY 830 gccacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 889
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 gccacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 100
QY 890 gacgagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 949
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 99 gacgagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 40
QY 950 aagcagatcccgatgagcttacttactgaagagcagcagcagcagcagcagcagcagc 988
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 39 aagcagatcccgatgagcttacttactgaagagcagcagcagcagcagcagcagcagc 1

```

```

RESULT 13
BF042944
LOCUS BF042944 362 bp mRNA EST 10-MAY-2000
DEFINITION BP250002A10F3 Soares normalized bovine placenta Bos taurus cDNA
clone BP250002A10F3 5', mRNA sequence.
ACCESSION BF042944
VERSION BF042944.1 GI:10759499
KEYWORDS EST.
SOURCE EST.
ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
            1 (bases 1 to 362)
AUTHORS Lewin, H.A., Soares, M.B., Rebholz, M., Pardinas, J., Liu, L. and Larson
            J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
            W. M. Keck Center for Comparative and Functional Genomics
            University of Illinois at Urbana-Champaign
            340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
            61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu

```

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross-match from Washington University Genome Center PHRAP suite.

Id.	Sequence	Position
14b	GGGGTTCAGGCTTTCTGCTGCTGGAAATATATATGAAATTACTCTGGAGGAGTTCCTAAC	240
17	GGTGTGATTAAGCTCTGATGATTTGGCTGGCTGATCATCTTTTAACTGATGATGAGTGA	702
19b	GCTGTGGTAAATAAAGAACTGATGGCTTTTGGCTAGCTGAGTATCTTTTATATATACGTAAATGCA	1000
27	GGTCTGGAGGATGGCTTTGATAGAGCTGGGCTCT	745
19b	TTCTTTTCAAGATAGCTTTTGATATAGACTTCAAGTCTC	333

Source: *China's Employment*, November 1995, 2(4):1, 15; 18; 17.
 Date: 11/19/95